

## FIGURE 1

Fucosyltransferase nucleotide sequence from strain 1182 FutB (SEQ ID NO:1)

atgttccaaccctattagacgcttatatagaagcgcttcattgaaaaattacctctaaatctccccccccctaaaaatcgctg  
tggcgaattggtggggagatgaagagggtgaagaatttaaaagaacattctttatttctcagtcagcattacacaatcacct  
ccacaaaaacccaacgaacctccgatctcgtcttggcagtcctattggatcagccagaaaaatctatcctatcaaacgcaa  
aaagagtgtttacaccgggtgaaacgaatcgctaatttcaacctcttgattacgccataggcttgatgaattggatttagagat  
cgttatttaagaatgcctttatattatgatagactacaccataaagccgagagcgtgaatgacaccacttcgcttacaactcaaac  
ctgacagccttatgctttaaaaaacccctccatcattttaaagaaaaccaccccaattatgcgcagtagtgaacaatgagagcg  
atcctttgaaaagagggttgcgagttttagcggagcaaccctaacgctcctaaaagggaatgctttctatgacgttttaattctata  
gagccagttattgggggagggagcgtgaaaaacacattaggctataacattaaaaacaagagcgagttttaagccaatacaaat  
tcaatctgtgtttgaaaactcacaaggctatggctatgtaactgaaaaatcattgacgcttacttagccataaccattcctattattg  
ggggagtcctagcgtggcacaagattttaaccctaagagtttggtaattgtgattttaagatttgatgaagcgattgatcatgt  
gcgatacttgcacacgcacccaaacgcttatttagacatgctttatgaaaacccttaaacaccctgatgggaaagcttactttac  
caaaatttgagtttaaaaaaatcctagattttttaaacgatttagaaaaacgacacgattatcacgataaccctttatttttctcgt  
gatttgaatgagccgttaatatctattgatgatgattgaggggtaattatgatgattgaggggtaattatgatgattgaggggtaatta  
tgatgattgaggggtaattatgatgattgaggggtaattatgatgattgaggggtaattatgatgattgaggggtaattatgatgatt  
gaggggtaattatgatgattgaggggtaattatgatgattgaggggtaattatgatgattgaggggtaattatgagcggctcttaca  
aaacgcctcgcctttattagaactctcctcaaacaccacattttaaatctatcgcaaagcttatcaaaaatccttaccttgttgcgtgc  
ggcgagaaagtgtgattaaaaaattgggttgtaa

Protein sequence from strain 1182 FutB (SEQ ID NO:2)

mfqplldayiesasiekitskspplkiavanwwgdeeevefknilyfilsqhytitlhqnpnepslvfgspigsarkilsy  
qnakrvfytgenespnfnlfdyaigfdeldfrdrylrmplydrllhkaesvndttspyklkpdsllyalkkpsghhfkennhpl  
cavvnnesdplkrgrfasfnpnkpnafydvlnsiepvigggsvkntlgyniknkseflsqyknfclfensqgygyvte  
kiidayfshtipiywgspsvaqdfnpksfsvncdfkdfdeaidhvrylhthpnayldmlyenplntldgkayfyqnlsfkki  
ldffktilendtiyhndpfifyrdlneplisiddlrvnyddlrvnyddlrvnyddlrvnyddlrvnyddlrvnyddlrvnydd  
lrvnyddlrvnyddlrvnyddlrvnyerllqnaspllelsqnttfkiyrkayqkslplraarklikklgl\*

## FIGURE 2

Fucosyltransferase from strain 1111 FutA

Nucleotide coding sequence (SEQ ID NO:3)

atgttccaaccctattagatgcctttatagaaagcgctccattgaaaaatggcctctaatactccccccctaaaaatcgctgtg  
cgaattggtggggagatgaagaaataaaaaatttaaaagagcgttcctttatcctaagccagcattacacaatcactttaca  
ccgaaacctgataaacctgcggacatcgctttgtaaccccttgatcagccagaaaaatctatcctatcaaacgcaaaaa  
gggtgtttacaccgggtgaaaatgaagtcctaactcaacctcttgattacgccataggcttgatgaattggacttta gagatcgt  
tatttgagaatgcctttgtattatgcctattgcattataaagccgagcttgtaatgacaccactcgccttataaacccaacctgaca  
gcctttatgctttaaaaaaacctcccatcatttaagaaaaccacccaatttgcgcgagtagtgaataatgagagtgatccttg  
aaaagaggggttgcgagcttggcgaagcaaccctaacgctcctagaaggaacgcttttatgagccttaaacgctattgagcc  
agttgctgggggaggggagcgtgaaaaacacattaggctataatgtcaaaaacaagagcgcgagttttaagccaatacaaatcaat  
ctgtgtttgaaaacacicaaggctatggctatgtaactgaaaagatcattgacgcttattcagccataccattcctattattggggg  
agtcccagcgtggcgaaagattttaaccctaagagtttgaatgtccatgattcaacaacttgatgaagcgattgactatatca  
gatacttgacacgcacccaaacgcttatttagacatgcactatgaaaacccttaaacactattgatgggaaagcttactttacca  
aaatttgagtttaaaaaaatcctagatttttaaaacgattttgaaaacgacacgatctatcacgataacccttcattttctatcgtg  
atttgaatgagccttcagtatctattgatggttgagggttaattatgatgattgagggttaattatgatgattgagggttaattatgat  
gattgagggttaattatgagcgcctttacaaaacgcctcgcctttattagaactctctcaaacaccacttttaaatctatcgcaaa  
gcttatcaaaaatccttgcctttgttgcgtgccataaggagatgggttaaaaagtaa

Protein sequence (SEQ ID NO:4)

mfpplldafiesaplkkwplnlpplkiavanwwgdeeikkfkksvlyfilsqhytitlhrnpdkpadivfgnplgsarkilsy  
qnakrvfytgenevpnfnlfdyaigfdeldfrdrylrmpllyaylhykaelvndttspyklqpdsllyalkkpshhfkcnhpn  
lcavvnnesdplkrfsvasnpnaprrnafyealnaiepvagggsvkntlgynvknkseflsqyknfclcfentqgygyvt  
ekiidayfshtipiywgspsvakdfnpksfvnvhdfnfdeaidyirylhthpnayldmhyenplntidgkayfyqnlsfk  
kildffktilendtiyhdnpfifyrdlnepsvsidglrvnyddlrnyddlrnyddlrnyerllqnaspllelsqnttfkiyrka  
yqkslpplrairrwvkk\*

## FIGURE 3

Strain 1218 FutB nucleotide sequence (SEQ ID NO:5)

atgttccaaccctattagacgcttatatagaagcgctccattgaaaaattacctctaaatctcccccccccctaaaaatcgctg  
tggcgaattggtggggagatgaagagggtgaagaatttaaaagaacattctttatttctcagtcagcattacacaatcacct  
ccacaaaacccaacgaacctccgatcgtcttggcagtcctattggatcagccagaaaaatctatcctatcaaacgcaa  
aaagagtgtttacaccgggtgaaacgaatgcctaattcaacctcttgattacgccataggcttgatgaattggatttagagat  
cgttattaagaatgcctttatattatgatagactacaccataaagccgagagcgtgaatgacaccacttcgcttacaaactcaaac  
ctgacagcctttatgctttaaaaaaacctcccatcattttaaagaaaaccacccaatttatgcgcagtagtgaacaatgagagcg  
atcctttgaaaagagggttgcgagttttagcgcagcaacctaacgctcctaaaagggaatgcttctatgacgcttaaatctata  
gagccagttattgggggaggagcgtgaaaaacaccttaggctataacattaaaaacaagagcgagttttaagccaatacaaat  
tcaatctgttttgaaaactcacaaggctatggctatgtaactgaaaaatcattgacgcttacttagccataaccattcctatttg  
ggggagtcttagcgtggcacaagatttaaccctaagagtttgaatgtttgattttaaagattttgatgaagcgattgatcatgt  
gcgatacttgacacgcacccaacgcttatttagacatgccttatgaaaaccccttaaacacccctgatgggaaagcttactttac  
caaaatttgagtttaaaaaatcctagattttttaaacgatcttagaaaacgacacgattatcacgataaccctttattttatcgt  
gatttgaatgagccgttaatatctattgatgattgagggttaattatgatgattgagggttaattatgatgattgagggttaattatga  
tgattgagggttaattatgatgattgagggttaattatgatgattgagggttaattatgatgattgagggttaattatgatgattga  
gggttaattatgatgattgagggttaattatgatgattgagggttaattatgatgattgagggttaattatgatgagcggtcttaca  
acgcctgcctttattagaactctctcaaacaccacttttaaatctatcgcaagcttatcaaaaatccttaccttggcgtgcgg  
cgagaaagtgattaaaaaattgggtttaa

Predicted protein strain 1218 FutB (SEQ ID NO:6)

mfqplldayiesasiekitskppplkiavanwwgdeeeefkknilyfilsqhytitlhqnpnepsdlvfgspigsarkilsy  
qnakrvfytgenespnfnldyaigfdeldfrdrylrmplyydrhhkaesvndtspyklkpdsllyalkkpshhfknhpnl  
cavvnesdplkrqfasfvasnnpakrnafydaalnsiepvigggsvkntlgyniknkseflsqyknfclfensqgygyvte  
kiidayfshtipiywgspsvaqdfnpksfvnvcdfkdfdaidhvrylhthpnayldmlyenplntldgkayfyqnlsfkki  
ldffktilendtiyhdnpfifyrdlneplisiddlrnyddlrnyddlrnyddlrnyddlrnyddlrnyddlrnyddlrnyddlr  
vnyddlrnncddlrnyddlrnyerllqnaspllelsqnttfkiyrkayqkslprraarklikklgl\*

FIGURE 4

Fucosyltransferase strain 19C2 FutB nucleotide sequence (SEQ ID NO:7)

atgttccaaccctattagacgcttatatagacagcaccggttagatgaaaccgattataagccccattaaatatagccctagcg  
aattggtggcctttggataaaagagaaagcaaagggttagaaaaaatttattcttaccatttcattttaagtcagcattacacaatcgc  
tctccaccgaaaccctgataaacctgcggacatcgttttggtaaccccttgatcagccagaaaaatcctatcctatcaaacg  
ctaaaagggtgttttacaccggtgaaaacgaagtccttaattcaacctcttgattacgccataggctttgatgaattggactttaga  
gatcggtatttgagaatgcctttatattatgatagactacaccataaagccgagagcgtgaatgacaccaccgcacctacaagatt  
aaatctgacagcctttatgctttaaaaaagccctcccatcttttaagaaaaccacccacatttatgcgcgctaataataatgaga  
tcgatcctttgaaaagagggtttgcgagctttgtcgcaagcaaccctaacgccctataaggaacgctttctatgaggctttaattc  
tattgagccagttactgggggagggagcgtgagaacactttaaggctataacgtcaaaaacaaaaacgaattttgagccaatac  
aagtcaatctgtgctttgaaaacactcaaggctatggctatgttactgaaaaaatcattgacgcttactcagccacaccattcctat  
ttattgggggggagtccttagcgtggcgaaagattttaacccc

Strain 19C2 FutB protein sequence (SEQ ID NO:8)

mfqplldayidstrldetdykpplnialanwwpldkreskgfrkkfilhflsqhytialhrnpdkpdivfgnplgsarkilsy  
qnakrvfytgenevpfnlfdyaigfdeldfrdrylrmplyydrllhkaesvndttapykiksdslalkkpsghfkenhph  
lcalinneidplkrghfasfnpnapiamafyealnsiepvttggsvrmtlgynvknkneflsqyknlcfcntqgygyvtek  
iidayfshtipiyyggvpsvakdfnp

## FIGURE 5

Strain 915 FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:9)

atggcctctaaatctccccctaaaaatcgctgtggcgaattggtggggagatgaagaaattaaaaattaaaaagagcgttct  
ttattttatcctaagccagcattacacaatcactttacaccgaaaccctgataaacctgcggacatcgtctttgtaaccccttggat  
cagccagaaaaatcttatcctatcaaaacgaaaaagggtgtttacaccggtgaaaatgaagtcctaactcaaccttttgatta  
cgccataggctt

Protein sequence from Strain 915 FutA (SEQ ID NO:10)

maskspplkiavanwwgdeeikkfkksvlyfilsqhytitlhmpdkpadi vfgnplgsarkilsyqnakrvfytgenevnpn  
fnlfdaigf

FIGURE 6

Strain 26695 FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:11)

atgttccaaccctattagacgcctttatagaagcgcttcattgaaaaatggcctctaaatctccccccccccctaaaaatc  
gctgtggcgaattggtggggagatgaagaaattaaagaatttaaaaagagcgttctttttatcctaagccaacgetacgcaatc  
accctccacaaaaccccaatgaatttcagatctagtttttagcaatcctcttgagcggctagaaagatttatcttataaaacac  
taaacgagtggtttacaccgggtgaaaacgaatcacctaatttcaacctcttgattacgccataggctttgatgaattggattttaatga  
tcgttattgagaatgccttgtattatgccatttgcactataaagccgagcttgtaatgacaccactgcgcctacaaactcaaag  
acaacagcctttatgctttaaaaaacccctctcatctttaaagaaaaccaccctaatttgcgcagtagtgatgatgagagcg  
atcttttaaaaagagggtttgccagtttttagcgagcaacgctaacgctcctatgaggaacgcttttatgacgctctaaattccata  
gagccagttactgggggaggaagtgtgagaacactttaaggctataaggttggaacaaaagcgagttttaagccaataacaagt  
tcaatctctgtttgaaaactgcgaaggttatggctatgaaccgaaaaatccttgatgcgtatttagccataaccattctatttattg  
ggggagtcccagcgtggcgaaagattttaaccctaaaagtttgtgaatgtgcatgattcaacaactttgatgaagcgattgattat  
atcaaatacctgcacacgcacccaaacgcttatttagacatgctctatgaaaaccctttaaacacccttgatgggaaagccttacttt  
accaagatttgagtttaaaaaaatcctagattttttaaacgattttagaacgatacgatttatcacaattctcaacatcttcatg  
tgggagtacgatctgcataagccgtagtatccattgatgattgaggggttaattatgatgattgaggggttaattatgaccggccttta  
caaacgcttcgcctttattagaactctctcaaacaccacttttaaaatctatcgcaaagccttatcaaaaatccttgcccttgttgcgc  
gcggtgagaaagttggttaaaaaattgggttgtaa

Protein coding sequence Strain 26695 FutA (SEQ ID NO:12)

mfqplldafiesasiekmaskspplkiavanwwgdeeikefkksvlyfilsqryaitlhqnpnefsdlvfnplgaarkil  
syqntkrvfytgenespnfnlfdyaigfdeldfndrylrmpllyahlykaelvndttapyklkdnslyalkkpshhfkenn  
pnlcavvndesdllkrghasfvasnanapmrnafydaalnsieptvggsvrntlgkvgnkseflsqyknlfensqgygy  
vtekildayfshtipiywgspsvakdfnpksfvnvhdfnfdeaidyikylhthpnayldmlyenplntldgkayfyqdlf  
kkildffktilendtiyhkfstsfnweydlhkplvsiddlrnyddlrnydrllqnaspllelsqnttfkiyrkayqkslplrav  
rkivkkgl\*

FIGURE 7

19C2A fucosyltransferase nucleotide sequence (SEQ ID NO:13)

atgtccaacccttactagacgcctttatagaaagtgctccaatt

19C2A predicted protein sequence (SEQ ID NO:14)

mfqplldafiesapi

## FIGURE 8

Protein sequence from strain 1182 FutB aligned with pfam00852, Glyco\_transf\_10, Glycosyltransferase family 10

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Query: 23 PPPLKIAVANWWGDDEEVEEFKKNILYFILSQHYTTITLHQNPNEPSDLVFGS-PIGSARKI 81
Sbjct: 11 TVPLLLAIYTWWSLIEYKEWKKSPIYFIGSQAPQPPLR---ILLWTWPFNGNPLALSDCP 67

Query: 82 LSYQNAKRVFYTGEN---ESPNFNLF---DYAIGFDELDFRDRYLRMPLYDRLHHKAES 135
Sbjct: 68 LSYQNTARCRLTANRSPLESDAVLFHHRDLKSGFPDLPPSPRPPGQPWVWASMESPSNS 127

Query: 136 -VNDTTSPIYKLKPDLSLYALKKPSHHFKENHPNLCAVVNNESDPLKRGFASFVASNPN-AP 193
Sbjct: 128 GLNDLRDGYFNWTLSTYRADSDAFHPYGYLEPRLSQVVNAPLLSAKRKGAAWVVSNCNTRS 187

Query: 194 KRNAFYDVLNSIEPVIGGGSVKNTLGYNINKKSEFLSQYKFNLCFENSQGYGYVTEKIID 253
Sbjct: 188 KRERFYKQLNKHQLQVDVGGRVANPLPLKVGCLVETLSQYKFYLAFENSQHYDYVTEKLWK 247

Query: 254 -AYFSHTIPIYWGSPSVAQDFNP-KSFVNVCDFKDFDEAIDHVRYLHTHPNAYL 305
Sbjct: 248 NALQAGTIPVVLGPRAVYEDFVPPKSFIVHDDFKSPKELADYLLYLDTNPTAYS 301

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## FIGURE 9

Fucosyltransferase from strain 1111 FutA aligned with pfam00852, Glyco\_transf\_10,  
Glycosyltransferase family 10

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Query:  27  IAVANWWGDEEIKKFKKSVLYFILSQHYTITLHRNPDKPADIVFG-NPLGSARKILSYQN' 85
Sbjct:  16  LAIYTWWSLIEYKEWKKSPIYFIGSQAPQPPLR---ILLWTWPFNGNPLALSDCPLSYQN 72

Query:  86  AKRVFYTGGEN---EVPNFNLF---DYAIGFDELDFRDRYLRMPLYAYLHYKAEL-VNDT 138
Sbjct:  73  TARCLRTANRSPLESADAVLFHHRDLSKGFEDLPPSPRPFGQPWWASMESPSNSGLNDL 132

Query:  139  TSPYKLQPDLSLYALKKPSHHFKENHENLCAVVNNESDPLKRGFASFVASNPN-APRRNAF 197
Sbjct:  133  RDGYFNWTLSTYRADSDAFHPYGYLEFRLSQVVNAPLLSAKRKGAAWVVSNCNTRSKRERF 192

Query:  198  YEALNAIEPVAGGGSVNTLGYNVKNKSEFLSQYKFNLCFENTQGYGYVTEKIID-AYFS 256
Sbjct:  193  YKQLNKHLQVDVGGRVANPLPLKVGCLVETLSQYKFYLAFENSQHYDYVTEKLWKNALQA 252

Query:  257  HTIPIYWGPSVAKDFNP-KSFVNVHDFNNFDEAIDYIRYLHTHPNAYLDMHYENPLNTI 315
Sbjct:  253  GTIPVVLGPRAVYEDFVPPKSFHVDDFKSPKELADYLLYLDTNPTAYS----- 301

Query:  316  DGKAYFYQNLSFKKILDFFKTILENDTIYHDNPFIFYRDLNEPSVSIIDGLRVNYDDLVRN 375
Sbjct:  302  -----EYFEWRYDLRVRLFSWDALR----- 321

Query:  376  YDDLVRNYDDLVRVNYERLLQNASPLLELSQNTTFKIYRKAYQ 417
Sbjct:  322  -----YDEGFCRVCRLLOQAPD-----RYKTYPNIAKWFQ 351

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## FIGURE 10

Protein sequence from strain 1218 FutB aligned with pfam00852, Glyco\_transf\_10,  
Glycosyltransferase family 10

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Query: 23 PPPLKIAVANWVGDEEVEEFKKNILYFILSQHYTITLHQNPNEPSDLVFGS-PIGSARKI 81
Sbjct: 11 TVPLLLAIYTWWSLIEYKEWKKSPIYFIGSQAPQPPLR---ILLWTWPFNGNPLALSDCP 67

Query: 82 LSYQNAKRVFYTGEN---ESPNNLF---DYAIGFDELDFRDYLRMPLYYDRLHHKAES 135
Sbjct: 68 LSYQNTARCRLTANRSPLESADAVLFHHRDLKSGFDLPSPRPFGQPWWWASMESPSNS 127

Query: 136 -VNDTTSFYKLPDSLYALKKPSHHFKENHPNLCAVVNNESDPLKRGFASFVASNPN-AP 193
Sbjct: 128 GLNDLRDGYFNWTLSTYRADSDAFHPYGYLSPRLSQVVNAPLLSAKRKGAAWVVSNCNTRS 187

Query: 194 KRNAFYDALNSIEPVIIGGGSVKNTLGYNIKNKSRLSQYKFNLCPENSQGYGYVTEKIID 253
Sbjct: 188 KRERFYKQLNKLQVDVGGRVANPLPLKVGCLVETLSQYKFYLAFENSQHYDYVTEKLWK 247

Query: 254 -AYFSHTIPIYWGSPPVAQDFNP-KSFVNVCDFKDFDEAIDHVRYLHTHPNAYLDMLYEN 311
Sbjct: 248 NALQAGTIPVVLGPRAVYEDFVPPKSFHVDVDFKSEKELADYLLYLDTNPTAYS----- 301

Query: 312 PLNTLDGKAYFYQNLSEFKILDFFKTILENDTIYHDNPFIFYRDLNEPLISIDDLRVNYD 371
Sbjct: 302 -----EYFEWRYDLRVRLFSDALR--YD 323

Query: 372 DLRVNYDDL RVNYDDL RVNYDDL RVNYD 399
Sbjct: 324 EGFCRVCRLQLNAPDRYKTYPNIAKWFO 351

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## FIGURE 11

Protein sequence from strain 19C2 FutB aligned with pfam00852, Glyco\_transf\_10,  
Glycosyltransferase family 10

```

Query:  22  PPLNIALANWWPLDKRESKGFRKKFILHFIILSQHYTIALHRNPDKPADIVFG-NPLGSAR  80
Sbjct:  12  VPLLLAIYTWWSL--IEYKEW-KKSPIYFIGSQAPQPPLR---ILLWTWPFNGNPLALSD  65

Query:  81  KILSYQNAKRIFYTGEN---EVFNFNLF---DYAIGFDELDPRDRYLRLPLYDRLHHKA  134
Sbjct:  66  CPLSYQNTARCRLTANRSPLESADAVLFHHRDLKSGFFDLPPSPRPPGQFWVWASMESPS  125

Query:  135  ES-VNDITAFYKIKSDSLYALKKPSHHFKENHPLCALINNEIDPLKRGFASFVASNPN-  192
Sbjct:  126  NSGLNLDLRDGYFNWTLSTYRADSDAFHPYGYLEPRLSQVVNAPLLSAKRKGAAWVVSNCNT  185

Query:  193  APIRNAFYEALNSIEPVTGGGSVRNTLGYNVKNKNEFLSQYKFNLCPENTQGYGYVTEKI  252
Sbjct:  186  RSKRERFYKQLNKLQVDVGGGRVANPLPLKVGCLVETLSQYKFYLAPEHSQHYDYVTEKL  245

Query:  253  ID-AYFSHTIPIYWGGVPSVAKDFNP  277
Sbjct:  246  WKNALQAGTIPVVLGP-RAVYEDFVP  270

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FIGURE 12

	1		50
1111FutA.pep	(1)	MFQPLLDAFIESAPKKWPLN--LPPLKIAVANWWGDEETKK---FKKSM	
19C2A.pep	(1)	MFQPLLDAFIESAPI-----	
915A.pepneose	(1)	-----MASK-SPPLKIAVANWWGDEETKK---FKKSM	
26695A.pep	(1)	MFQPLLDAFIESASIEKMASKSPPPPLKIAVANWWGDEETKE---FKKSM	
1182B.pep	(1)	MFQPLLDAYIESASIEKITSKS-PPPLKIAVANWWGDEEVBEE---FKKNT	
1218B.pep	(1)	MFQPLLDAYIESASIEKITSKS-PPPLKIAVANWWGDEEVBEE---FKKNT	
ORF19C2B.pep	(1)	MFQPLLDAYIDSTRIDETDYK--PELNIAVANWWPLDKRESKGFRKKFI	
Consensus	(1)	MFQPLLDAFIESA IEK SK PPLKIAVANWWGDEEI FKK I	
	51		100
1111FutA.pep	(46)	LYFILSQHYTITLHRNPDKPADIVFGNPLGSARKILSYONAKRVFYTGEN	
19C2A.pep	(16)	-----	
915A.pepneose	(29)	LYFILSQHYTITLHRNPDKPADIVFGNPLGSARKILSYONAKRVFYTGEN	
26695A.pep	(48)	LYFILSQRYAITLHQNPNFESDEVFSNPLGSARKILSYONTKRVFYTGEN	
1182B.pep	(47)	LYFILSQHYTITLHQNPNFESDHFVGSPLGSARKILSYONAKRVFYTGEN	
1218B.pep	(47)	LYFILSQHYTITLHQNPNFESDHFVGSPLGSARKILSYONAKRVFYTGEN	
ORF19C2B.pep	(48)	LYFILSQHYTITLHRNPDKPADIVFGNPLGSARKILSYONAKRVFYTGEN	
Consensus	(51)	LYFILSQHYTITLH NP PADIVFGNPLGSARKILSYONAKRVFYTGEN	
	101		150
1111FutA.pep	(96)	EVPNFNLFDYAIGFDELDFRDRYLRMPLYYAHLLHKAELVNDTTSFYKLG	
19C2A.pep	(16)	-----	
915A.pepneose	(79)	EVPNFNLFDYAIGF-----	
26695A.pep	(98)	ESPNFNLFDYAIGFDELDFNDRYLRMPLYYAHLLHKAELVNDTTSFYKLG	
1182B.pep	(97)	ESPNFNLFDYAIGFDELDFRDRYLRMPLYYDRLLHKAESVNDTTSFYKLG	
1218B.pep	(97)	ESPNFNLFDYAIGFDELDFRDRYLRMPLYYDRLLHKAESVNDTTSFYKLG	
ORF19C2B.pep	(98)	EVPNFNLFDYAIGFDELDFRDRYLRMPLYYDRLLHKAESVNDTTSFYKLG	
Consensus	(101)	E PNFNLFDYAIGFDELDFRDRYLRMPLYY LHHKAE VNDTTSFYKLG	
	151		200
1111FutA.pep	(146)	PDSLYALKKPSHHFKENHPNLCAVVNNESEDPLKRGFASFVASNPNAIRN	
19C2A.pep	(16)	-----	
915A.pepneose	(93)	-----	
26695A.pep	(148)	DNSLYALKKPSHHFKENHPNLCAVVNNESEDLLKRGFASFVASNANAPMRN	
1182B.pep	(147)	PDSLYALKKPSHHFKENHPNLCAVVNNESEDPLKRGFASFVASNPNAIRN	
1218B.pep	(147)	PDSLYALKKPSHHFKENHPNLCAVVNNESEDPLKRGFASFVASNPNAIRN	
ORF19C2B.pep	(148)	SDSLYALKKPSHHFKENHPNLCAVVNNESEDPLKRGFASFVASNPNAIRN	
Consensus	(151)	DSLYALKKPSHHFKENHPNLCAVVNNESEDPLKRGFASFVASNPNAIRN	
	201		250
1111FutA.pep	(196)	AFYEALNSTIEPVAGGGSVKNTLGYNVKNKSEFLSQYKFNLCFENSGQYGY	
19C2A.pep	(16)	-----	
915A.pepneose	(93)	-----	
26695A.pep	(198)	AFYDALNSTIEPVTGGGSVKNTLGYSKKNKSEFLSQYKFNLCFENSGQYGY	
1182B.pep	(197)	AFYDVLNSTIEPVIGGGSVKNTLGYNVKNKSEFLSQYKFNLCFENSGQYGY	
1218B.pep	(197)	AFYDALNSTIEPVIGGGSVKNTLGYNVKNKSEFLSQYKFNLCFENSGQYGY	
ORF19C2B.pep	(198)	AFYEALNSTIEPVTGGGSVKNTLGYNVKNKSEFLSQYKFNLCFENSGQYGY	
Consensus	(201)	AFYDALNSTIEPV GGGSVKNTLGYNVKNKSEFLSQYKFNLCFENSGQYGY	

FIGURE 13

	1	50
1111FutA	(1) ATGTTCCAACCCCTATTAGATGCCTTTATAGAAAGCGCT-CCATTGAAAA	
915A.cod (MWG)	(1) ATGTTCCAACCCCTATTAGATGCCTTTATAGAAAGCGCTTCCATTGAAAA	
19C2FutA.cod	(1) ATGTTCCAACCCCTACTAGACGCCTTTATAGAAAGTGCTCCAATT-----	
26695A.cod	(1) ATGTTCCAACCCCTATTAGACGCCTTTATAGAAAGCGCTTCCATTGAAAA	
1182B	(1) ATGTTCCAACCCCTATTAGACGCCTTTATAGAAAGCGCTTCCATTGAAAA	
1218B.nuc	(1) ATGTTCCAACCCCTATTAGACGCCTTTATAGAAAGCGCTTCCATTGAAAA	
ORF19C2B	(1) ATGTTCCAACCCCTATTAGACGCCTTTATAGACAGCACCCGTTTAGATGA	
Consensus	(1) ATGTTCCAACCCCTATTAGACGCCTTTATAGAAAGCGCTTCCATTGAAAA	
	51	100
1111FutA	(50) AATGGCCTCTAAATCTCCCCCCC-----TAAAAATCGCTGTGGCGAATT	
915A.cod (MWG)	(51) AATGGCCTCTAAATCTCCCCCCC-----TAAAAATCGCTGTGGCGAATT	
19C2FutA.cod	(46) -----	
26695A.cod	(51) AATGGCCTCTAAATCTCCCCCCCCCCCCCTAAAAATCGCTGTGGCGAATT	
1182B	(51) AATTACCTCTAAATCTCCCCCCCCCCC-----TAAAAATCGCTGTGGCGAATT	
1218B.nuc	(51) AATTACCTCTAAATCTCCCCCCCCCCC-----TAAAAATCGCTGTGGCGAATT	
ORF19C2B	(51) AACCGATTATAA-----GCCCCCAT---TAAATATAGCCCTAGCGAATT	
Consensus	(51) AAT GCCTCTAAATCTCCCCCCC TAAAAATCGCTGTGGCGAATT	
	101	150
1111FutA	(95) GGTGG-----GGAGATGA-AGAAATTAAAAATTTAAAAAGAGCCTTCTTT	
915A.cod (MWG)	(95) GGTGG-----GGAGATGA-AGAAATTAAAAATTTAAAAAGAGCCTTCTTT	
19C2FutA.cod	(46) -----	
26695A.cod	(101) GGTGG-----GGAGATGA-AGAAATTAAAAAGATTTAAAAAGAGCCTTCTTT	
1182B	(98) GGTGG-----GGAGATGA-AGAGGTGGAAGATTTAAAAAGAGATTTCTTT	
1218B.nuc	(98) GGTGG-----GGAGATGA-AGAGGTGGAAGATTTAAAAAGAGATTTCTTT	
ORF19C2B	(92) GGTGGCCTTTGGATAAAAGAGAAAGCAAAGGGTTTAGAAAAAATTTATC	
Consensus	(101) GGTGG GGAGATGA AGAAATTAAAGATTTAAAAAGA C TTCTT	
	151	200
1111FutA	(139) T---ATTTTATCCTAAGCCAGCATTACACAATCAGTTTACACCGAAACCC	
915A.cod (MWG)	(139) T---ATTTTATCCTAAGCCAGCATTACACAATCAGTTTACACCGAAACCC	
19C2FutA.cod	(46) -----	
26695A.cod	(145) T---ATTTTATCCTAAGCCAAAGCTACGCAATCAGCCTGACCAAAACCC	
1182B	(142) T---ATTTTATTTCTCAGTCAGCATTAGACAATCAGCCTGACCAAAACCC	
1218B.nuc	(142) T---ATTTTATTTCTCAGTCAGCATTACACAATCAGCCTGACCAAAACCC	
ORF19C2B	(142) TTACATTTTATTTTAAAGTCAGCATTACACAATCAGTCTCCACCGAAACCC	
Consensus	(151) T ATTTTAT CTAAG CAGCATTACACAATCAC CTCCACC AAACCC	
	201	250
1111FutA	(186) TGATAAACCTGCGGACATCGTCTTTGGTAACCCCTTGGATCAGCCAGAA	
915A.cod (MWG)	(186) TGATAAACCTGCGGACATCGTCTTTGGTAACCCCTTGGATCAGCCAGAA	
19C2FutA.cod	(46) -----	
26695A.cod	(192) CAATGAATTTTCAGATCTAGTTTITAGCAATCCTCTTGGAGCGGCTAGAA	
1182B	(189) CAACGAACCCCTCCGATCTCGTCTTTGGCAGTCCTATTGGATCAGCCAGAA	
1218B.nuc	(189) CAACGAACCCCTCCGATCTCGTCTTTGGCAGTCCTATTGGATCAGCCAGAA	
ORF19C2B	(192) TGATAAACCTGCGGACATCGTCTTTGGTAACCCCTTGGATCAGCCAGAA	
Consensus	(201) AT AACCT C GA TCGTCTTTGG AA CC CTTGGATCAGCCAGAA	

## FIG. 13 (CONT)

	251	300
1111FutA	(236)	AAATCTTATCCTATCAAAACGCAAAAAGGGTGTTTTACACCGGTGAAAAT
915A.cod (MWG)	(236)	AAATCTTATCCTATCAAAACGCAAAAAGGGTGTTTTACACCGGTGAAAAT
19C2FutA.cod	(46)	-----
26695A.cod	(242)	AGATTTTATCCTTATCAAAACACTAAACGAGTGTTTTACACCGGTGAAAAC
1182B	(239)	AAATCTTATCCTATCAAAACGCAAAAAGAGTGTTTTACACCGGTGAAAAC
1218B.nuc	(239)	AAATCTTATCCTATCAAAACGCAAAAAGAGTGTTTTACACCGGTGAAAAC
ORF19C2B	(242)	AAATCCTATCCTATCAAAACGCTAAAAGGGTGTTTTACACCGGTGAAAAC
Consensus	(251)	AAATCTTATCCTATCAAAACGCAAAAAG GTGTTTACACCGGTGAAAAC
	301	350
1111FutA	(286)	GAAGTCCCTAACTTCAACCTCTTTGATTACGCCATAGGCTTT-GATGAAT
915A.cod (MWG)	(286)	GAAGTCCCTAACTTCAACCTCTTTGATTACGCCATAGGCTTTTATGATGA--
19C2FutA.cod	(46)	-----
26695A.cod	(292)	GAATCACCTAATTTCAACCTCTTTGATTACGCCATAGGCTTT-GATGAAT
1182B	(289)	GAATCGCCTAATTTCAACCTCTTTGATTACGCCATAGGCTTT-GATGAAT
1218B.nuc	(289)	GAATCGCCTAATTTCAACCTCTTTGATTACGCCATAGGCTTT-GATGAAT
ORF19C2B	(292)	GAAGTCCCTAATTTCAACCTCTTTGATTACGCCATAGGCTTT-GATGAAT
Consensus	(301)	GAA CCTAATTTCAACCTCTTTGATTACGCCATAGGCTTT GATGAAT
	351	400
1111FutA	(335)	TGGACTTTAGAGATCGTTATTTGAGAATGCCCTTTGTATTATGCCTATTITG
915A.cod (MWG)	(334)	-----
19C2FutA.cod	(46)	-----
26695A.cod	(341)	TGGATTTTAATGATCGTTATTTGAGAATGCCCTTTGTATTATGCCCATTTTG
1182B	(338)	TGGATTTTAGAGATCGTTATTTAAGAATGCCCTTTATATTATGATAGACTA
1218B.nuc	(338)	TGGATTTTAGAGATCGTTATTTAAGAATGCCCTTTATATTATGATAGACTA
ORF19C2B	(341)	TGGACTTTAGAGATCGTTATTTGAGAATGCCCTTTATATTATGATAGACTA
Consensus	(351)	TGGA TTTAGAGATCGTTATTT AGAATGCCCTT TATTATG T
	401	450
1111FutA	(385)	CATTATAAAGCCGAGCTTGTTAATGACACGCACTTCGCCTTATAAACTCCA
915A.cod (MWG)	(334)	-----
19C2FutA.cod	(46)	-----
26695A.cod	(391)	CACATATAAAGCCGAGCTTGTTAATGACACCACTGCCCTTACAAACTCAA
1182B	(388)	CACCATAAAGCCGAGAGCGTGAAATGACACCACTTCGCCTTACAAACTCAA
1218B.nuc	(388)	CACCATAAAGCCGAGAGCGTGAAATGACACCACTTCGCCTTACAAACTCAA
ORF19C2B	(391)	CACCATAAAGCCGAGAGCGTGAAATGACACCACTTCGCCTTACAAACTCAA
Consensus	(401)	CAC ATAAAGCCGAG GT AATGACACCACT CGCCTTACAAACTCAA
	451	500
1111FutA	(435)	ACCTGACAGCCTTTATGCTTTAAAAAAACCCCTCCCATCATTTTAAAGAAA
915A.cod (MWG)	(334)	-----
19C2FutA.cod	(46)	-----
26695A.cod	(441)	AGACAACAGCCTTTATGCTTTAAAAAAACCCCTCTCATCATTTTAAAGAAA
1182B	(438)	ACCTGACAGCCTTTATGCTTTAAAAAAACCCCTCCCATCATTTTAAAGAAA
1218B.nuc	(438)	ACCTGACAGCCTTTATGCTTTAAAAAAACCCCTCCCATCATTTTAAAGAAA
ORF19C2B	(441)	ATCTGACAGCCTTTATGCTTTAAAAAAACCCCTCCCATCATTTTAAAGAAA
Consensus	(451)	A CTGACAGCCTTTATGCTTTAAAAAAACCCCTCCCATCATTTTAAAGAAA

## FIG. 13 (CONT)

	501	550
1111FutA	(485) ACCACCCCAATTTGTGCGCAGTAGTGAATAATGAGAGTGATCCTTTTGAAA	
915A.cod (MWG)	(334) -----	
19C2FutA.cod	(46) -----	
26695A.cod	(491) ACCACCCCTAATTTGTGCGCAGTAGTGAATGATGAGAGCGATCTTTTAAAA	
1182B	(488) ACCACCCCAATTTATGCGCAGTAGTGAACAATGAGAGCGATCCTTTTGAAA	
1218B.nuc	(488) ACCACCCCAATTTATGCGCAGTAGTGAACAATGAGAGCGATCCTTTTGAAA	
ORF19C2B	(491) ACCACCCACATTTATGCGCGCTAATCAATAATGAGATCGATCCTTTTGAAA	
Consensus	(501) ACCACCC AATTT TGCAGTAGTGAA AATGAGAGCGATCCTTTTGAAA	
	551	600
1111FutA	(535) AGAGGGTTTGGCAGCTTTGTGCGCAAGCAACCCCTAACGCTCCTAGAGGAA	
915A.cod (MWG)	(334) -----	
19C2FutA.cod	(46) -----	
26695A.cod	(541) AGAGGGTTTGGCAGCTTTGTAGCGAGCAACGCTAACGCTCCTATGAGGAN	
1182B	(538) AGAGGGTTTGGCAGCTTTGTAGCGAGCAACCCCTAACGCTCCTAAAAGGAA	
1218B.nuc	(538) AGAGGGTTTGGCAGCTTTGTAGCGAGCAACCCCTAACGCTCCTAAAAGGAA	
ORF19C2B	(541) AGAGGGTTTGGCAGCTTTGTGCGCAAGCAACCCCTAACGCTCCTATAGGAA	
Consensus	(551) AGAGGGTTTGGCAG TTTGT GC AGCAACCCCTAACGCTCCTA AAGGAA	
	601	650
1111FutA	(585) CGCTTTTATGAGGCTTTAAACGCTATTGAGCCAGTTGCTGGGGGAGGGA	
915A.cod (MWG)	(334) -----	
19C2FutA.cod	(46) -----	
26695A.cod	(591) CGCTTTTATGAGGCTTTAAATTCATAGAGCCAGTTACTGGGGGAGGAN	
1182B	(588) TGCTTTCTATGAGCTTTAAATTCATAGAGCCAGTTATTGGGGGAGGGA	
1218B.nuc	(588) TGCTTTCTATGAGGCTTTAAATTCATAGAGCCAGTTATTGGGGGAGGGA	
ORF19C2B	(591) CGCTTTCTATGAGGCTTTAAATTCATTGAGCCAGTTACTGGGGGAGGGA	
Consensus	(601) GCTTT TATGA GCTTTAAATTCAT GAGCCAGTTA TGGGGGAGGGA	
	651	700
1111FutA	(635) GCGTGAAAAACACTTTAGGCTATAATGTCAAAAACAAGAGCGAGTTTTTA	
915A.cod (MWG)	(334) -----	
19C2FutA.cod	(46) -----	
26695A.cod	(641) GTGTGAGAAACACTTTAGGCTATAAGGTTGGAAACAAAGCGAGTTTTTA	
1182B	(638) GCGTGAAAAACACTTTAGGCTATAACATTAAAAACAAGAGCGAGTTTTTA	
1218B.nuc	(638) GCGTGAAAAACACTTTAGGCTATAACATTAAAAACAAGAGCGAGTTTTTA	
ORF19C2B	(641) GCGTGAGAAACACTTTAGGCTATAACGTCAAAAACAAGAGCAATTTTTG	
Consensus	(651) GCGTGA AAACACTTTAGGCTATAA T AAAAACAA AGCGAGTTTTTA	
	701	750
1111FutA	(685) AGCCAATACAAATTCAATCTGTGTTTGGAAAACACTCAAGGCTATGGCTA	
915A.cod (MWG)	(334) -----	
19C2FutA.cod	(46) -----	
26695A.cod	(691) AGCCAATACAAAGTTCAATCTGTGTTTGGAAAACCTCGCAAGGTTATGGCTA	
1182B	(688) AGCCAATACAAATTCAATCTGTGTTTGGAAAACCTCACAAGGCTATGGCTA	
1218B.nuc	(688) AGCCAATACAAATTCAATCTGTGTTTGGAAAACCTCACAAGGCTATGGCTA	
ORF19C2B	(691) AGCCAATACAAAGTTCAATCTGTGCTTTGGAAAACACTCAAGGCTATGGCTA	
Consensus	(701) AGCCAATACAA TCAATCTGTGTTTGGAAAAC C CAAGGCTATGGCTA	

## FIG. 13 (CONT.)

	751	800
1111FutA	(735) TGTAACCGAAAAAGATCATTGACGCTTATTTAGCCATACCATTCTATTT	
915A. cod (MWG)	(334) -----	
19C2FutA. cod	(46) -----	
26695A. cod	(741) TGTAACCGAAAAAATCCTTGATGCGTATTTAGCCATACCATTCTATTT	
1182B	(738) TGTAACCGAAAAAATCATTGACGCTTACTTTAGCCATACCATTCTATTT	
1218B. nuc	(738) TGTAACCGAAAAAATCATTGACGCTTACTTTAGCCATACCATTCTATTT	
ORF19C2B	(741) TGTTACTGAAAAAATCATTGACGCTTACTTCAGCCACACCATTCTATTT	
Consensus	(751) TGTAACCGAAAAAATCATTGACGCTTA TT AGCCATACCATTCTATTT	
	801	850
1111FutA	(785) ATTGGGGG--AGTCC-CAGCGTGGCGAAAGATTTAACCCTAAGAGTTTT	
915A. cod (MWG)	(334) -----	
19C2FutA. cod	(46) -----	
26695A. cod	(791) ATTGGGGG--AGTCC-CAGCGTGGCGAAAGATTTAACCCTAAGAGTTTT	
1182B	(788) ATTGGGGG--AGTCC-TAGCGTGGCACAAGATTTAACCCTAAGAGTTTT	
1218B. nuc	(788) ATTGGGGG--AGTCC-TAGCGTGGCACAAGATTTAACCCTAAGAGTTTT	
ORF19C2B	(791) ATTGGGGGGGAGTCCCTAGCGTGGCGAAGATTTAACCC-----	
Consensus	(801) ATTGGGGG AGTCC AGCGTGGC AAGATTTTAACCCTAA AGTTTT	
	851	900
1111FutA	(832) GTGAATGTCCATGATTTCAACAACTTTGATGAAGCGATTGACTATATACAG	
915A. cod (MWG)	(334) -----	
19C2FutA. cod	(46) -----	
26695A. cod	(838) GTGAATGTGCATGATTTCAACAACTTTGATGAAGCGATTGATTATAACAA	
1182B	(835) GTGAATGTTTGTGATTTTAAAGATTTTGATGAAGCGATTGATCATGTGCG	
1218B. nuc	(835) GTGAATGTTTGTGATTTTAAAGATTTTGATGAAGCGATTGATCATGTGCG	
ORF19C2B	(832) -----	
Consensus	(851) GTGAATGT TGATTT AA A TTTGATGAAGCGATTGA AT T	
	901	950
1111FutA	(882) ATACTTGACACGACCCAAACGCTTATTTAGACATGCACTATGAAAACC	
915A. cod (MWG)	(334) -----	
19C2FutA. cod	(46) -----	
26695A. cod	(888) ATACCTGCACACGACCCAAACGCTTATTTAGACATGCTCTATGAAAACC	
1182B	(885) ATACTTGACACGACCCAAACGCTTATTTAGACATGCTCTATGAAAACC	
1218B. nuc	(885) ATACTTGACACGACCCAAACGCTTATTTAGACATGCTCTATGAAAACC	
ORF19C2B	(832) -----	
Consensus	(901) ATAC TGCACACGACCCAAACGCTTATTTAGACATGC TATGAAAACC	
	951	1000
1111FutA	(932) CTTTAAACACTATTGATGGGAAAGCTTACTTTTACC AAAATTTGAGTTTT	
915A. cod (MWG)	(334) -----	
19C2FutA. cod	(46) -----	
26695A. cod	(938) CTTTAAACACCCCTTGATGGGAAAGCTTACTTTTACC AAGATTTGAGTTTT	
1182B	(935) CTTTAAACACCCCTTGATGGGAAAGCTTACTTTTACC AAAATTTGAGTTTT	
1218B. nuc	(935) CTTTAAACACCCCTTGATGGGAAAGCTTACTTTTACC AAAATTTGAGTTTT	
ORF19C2B	(832) -----	
Consensus	(951) CTTTAAACAC TTGATGGGAAAGCTTACTTTTACC AA ATTTGAGTTTT	



## FIG. 13 (cont)

		1001		1050
1111FutA	(982)	AAAAAATCCTAGATTTTTTTTAAAACGATTTTAGAAAACGACACGATCTA		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(988)	AAAAAATCCTAGATTTTTTTTAAAACGATTTTAGAAAACGATACGATTTA		
1182B	(985)	AAAAAATCCTAGATTTTTTTTAAAACGATTTTAGAAAACGACACGATTTA		
1218B.nuc	(985)	AAAAAATCCTAGATTTTTTTTAAAACGATCTTAGAAAACGACACGATTTA		
ORF19C2B	(832)	-----		
Consensus	(1001)	AAAAAATCCTAGATTTTTTTTAAAACGAT TTAGAAAACGA ACGAT TA		
		1051		1100
1111FutA	(1032)	TCACGATAACCC-----TTTCATTTCCTATCGTGATTGAATGAGCGTT		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(1038)	TCACAAATTCTCAACATCTTTTCATGTGGGAGTACGATCTGCATAAGCCGT		
1182B	(1035)	TCACGATAACCC-----TTTATTTTTATCGTGATTGAATGAGCGTT		
1218B.nuc	(1035)	TCACGATAACCC-----TTTATTTTTATCGTGATTGAATGAGCGTT		
ORF19C2B	(832)	-----		
Consensus	(1051)	TCAC A C C TTT AT T A GAT TG AT AGCC T		
		1101		1150
1111FutA	(1076)	CAGTATCTATTGATGGT---TTGAGGGTTAATTATGATGATTGAGGGTT		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(1088)	TAGTATCCATTGATGAT---TTGAGGGTTAATTATGATGATTGAGGGTT		
1182B	(1079)	TAATATCTATTGATGATGATTGAGGGTTAATTATGATGATTGAGGGTT		
1218B.nuc	(1079)	TAATATCTATTGATGAT---TTGAGGGTTAATTATGATGATTGAGGGTT		
ORF19C2B	(832)	-----		
Consensus	(1101)	A TATC ATTGATG T TTGAGGGTTAATTATGATGATTGAGGGTT		
		1151		1200
1111FutA	(1123)	AATTATGATGATTGAGGGTTAATTATGATGATTGAGGGTTAATTATGA		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(1135)	AATTATGACCGGCTTTTACAAAACGCTTCGCCCTTATTAGAACTCTCTCA		
1182B	(1129)	AATTATGATGATTGAGGGTTAATTATGATGATTGAGGGTTAATTATGA		
1218B.nuc	(1126)	AATTATGATGATTGAGGGTTAATTATGATGATTGAGGGTTAATTATGA		
ORF19C2B	(832)	-----		
Consensus	(1151)	AATTATGA T AA T TTT G T T A		
		1201		1250
1111FutA	(1173)	GCGCCTTTTACAAAACGCTTCGCCCTTATTAGAACTCTCTCAAAACACCA		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(1185)	AAACACCACTTTTAAAATCTATCGCAAAGCTTATCAAAAATCCTTGCCCTT		
1182B	(1179)	TGATTTGAGGGTTAATTATGATGATTGAGGGTTAATTATGATGATTGGA		
1218B.nuc	(1176)	TGATTTGAGGGTTAATTATGATGATTGAGGGTTAATTATGATGATTGGA		
ORF19C2B	(832)	-----		
Consensus	(1201)	AA		

## Fig. 13 (cont)

		1251	1300
1111FutA	(1223)	CTTTTAAAATCTATCGCAAAGCTTATCAAAAATCCTTGCCTTTGTTGCGT	
915A.cod (MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(1235)	TGTTGCGCGCGGTGAGAAAGTTGGTTAAAAAATGGGTTTGTA-----	
1182B	(1229)	GGGTTAATTATGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAAT	
1218B.nuc	(1226)	GGGTTAATTATGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAAT	
ORF19C2B	(832)	-----	
Consensus	(1251)	T A A	
		1301	1350
1111FutA	(1273)	GCCATAAGGAGATGGGTTAAAAAGTAA-----	
915A.cod (MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(1279)	-----	
1182B	(1279)	TATGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAATTATGAGCG	
1218B.nuc	(1276)	TGTGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAATTATGAGCG	
ORF19C2B	(832)	-----	
Consensus	(1301)		
		1351	1400
1111FutA	(1300)	-----	
915A.cod (MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(1279)	-----	
1182B	(1329)	GCTCTTACAAAACGCCCTCGCCTTTATTAGAACTCTCTCAAAACACCACTT	
1218B.nuc	(1326)	GCTCTTACAAAACGCCCTCGCCTTTATTAGAACTCTCTCAAAACACCACTT	
ORF19C2B	(832)	-----	
Consensus	(1351)		
		1401	1450
1111FutA	(1300)	-----	
915A.cod (MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(1279)	-----	
1182B	(1379)	TTAAAATCTATCGCAAAGCTTATCAAAAATCCTTACCTTTGTTGCGTGCG	
1218B.nuc	(1376)	TTAAAATCTATCGCAAAGCTTATCAAAAATCCTTACCTTTGTTGCGTGCG	
ORF19C2B	(832)	-----	
Consensus	(1401)		
		1451	1483
1111FutA	(1300)	-----	
915A.cod (MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(1279)	-----	
1182B	(1429)	GCGAGAAAGTTGATTAAAAAATTGGGTTTGTA	
1218B.nuc	(1426)	GCGAGAAAGTTGATTAAAAAATTGGGTTTGTA	
ORF19C2B	(832)	-----	
Consensus	(1451)		

# Oligo Structures

Lacto-N-neo-Tetraose (LNnT)

Gal $\beta$ 1-4GlcNAc $\beta$ 1-3Gal $\beta$ 1-4Glc

Lacto-N-Fucopentaose III (LNFP III)

Gal $\beta$ 1-4GlcNAc $\beta$ 1-3Gal $\beta$ 1-4Glc

3  
|  
1 $\alpha$ Fucose

Fig. 14

# Linkage Analysis by GC/MS

The samples were methylated, hydrolyzed, reduced with sodium borodeuteride, acetylated and analyzed by GC/MS along with samples of LNT and LNF3.

- A Glc vs. Glc-NAc value close to 1 favors fucosylation of Glc-NAc.
- A Glc vs. Glc-NAc value close to 0 favors fucosylation of Glc

FIG. 15

<i>H. Pylori</i> Strain	Glc vs. Glc-NAc
915A2	0.982
19C2A5	0.040
1111A2	0.975
19C2B1	0.991
1182B3	0.983

# 1 Liter LNFIII Synthesis

FIG. 16

Batch Number	Resin Type	Total Yield	Actual Percent Recovery
1-02	MR3 $\text{NH}_4\text{HCO}_3$ column (1ml resin/1ml synthesis)	1.567 g	61%
2-02	MR3 $\text{NH}_4\text{HCO}_3$ column (1ml resin/1ml synthesis)	1.760 g	68%
3-02	Dowex1/Dowex 50 (2ml resin/1ml synthesis)	1.221 g	47%

FIG. 17

